



SEQUENCE LISTING

<110> Hauptmann, Rudolph  
Himmler, Adolph  
Maurer-Fogy, Ingrid  
Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for Them

<130> 98,385-H

<140> 09/899,422

<141> 2001-07-03

<150> 09/525,998

<151> 2000-03-15

<150> 08/383,676

<151> 1995-02-01

<150> 08/153,287

<151> 1993-11-17

<150> 07/821,750

<151> 1992-01-02

<150> 07/511,430

<151> 1990-04-20

<160> 87

<170> PatentIn Ver. 2.0

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<222> (1)..(1368)

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<221> sig\_peptide

<222> (1)..(87)

<220>

<221> misc\_feature

<222> (88)..(120)

<223> Portion of TNF-BP pro protein cleaved by extracellular proteases following secretion.

<220>

<221> misc\_feature

<222> (606)..(633)

<223> Portion of TNF-BP pro protein cleaved by

extracellular proteases following secretion.

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1 5 10 15				
gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct	96			
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro				
20 25 30				
cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa	144			
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys				
35 40 45				
tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa	192			
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys				
50 55 60				
gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac	240			
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp				
65 70 75 80				
tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc	288			
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu				
85 90 95				
aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg	336			
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val				
100 105 110				
gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg	384			
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg				
115 120 125				
aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc	432			
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe				
130 135 140				
aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag	480			
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu				
145 150 155 160				
aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa	528			
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu				
165 170 175				
aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg	576			
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr				
180 185 190				
aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca	624			
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser				
195 200 205				
ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt	672			
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu				

210	215	220	
tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys 225	230	235	720
tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu 245	250	255	768
ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser 260	265	270	816
ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val 275	280	285	864
ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys 290	295	300	912
ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly 305	310	315	960
gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn 325	330	335	1008
ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp 340	345	350	1056
act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro 355	360	365	1104
ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu 370	375	380	1152
atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag ggc Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln 385	390	395	1200
tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala 405	410	415	1248
acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly 420	425	430	1296
tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro 435	440	445	1344

ccc gcg ccc agt ctt ctc aga tga 1368  
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<212> PRT  
<213> Homo sapiens

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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255

Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
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Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
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Pro Ala Pro Ser Leu Leu Arg  
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1 5 10 15

att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys	20	25	30	96
cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser	35	40	45	144
ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys	50	55	60	192
tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp	65	70	75	240
cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp	85	90	95	288
agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly	100	105	110	336
acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys	115	120	125	384
cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn	130	135	140	432
tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu	145	150	155	480
aat Asn				483

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Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 35 40 45
Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 50 55 60

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
65 70 75 80

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
85 90 95

Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
100 105 110

Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
115 120 125

His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
130 135 140

Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu  
145 150 155 160

Asn

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<212> DNA

<213> Homo sapiens

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gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga 87  
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
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<211> 29

<212> PRT

<213> Homo sapiens

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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
20 25

<210> 7

<211> 33

<212> DNA  
<213> Homo sapiens

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<222> (1)..(33)

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Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg  
1 5 10

33

<210> 8  
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<400> 8  
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg  
1 5 10

<210> 9  
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<212> DNA  
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<220>  
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Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
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30

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<210> 11  
<211> 1334  
<212> DNA  
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ctggacagac cgagtcccgga aagccccag cactgccgtt gccacactgc cctgagccca 180  
aatgggcgag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233  
Met Gly Leu Ser Thr Val Pro  
1 5

gac ctg ctg cta ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281  
Asp Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr  
10 15 20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329  
Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys  
25 30 35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377  
Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn  
40 45 50 55

tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425  
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
60 65 70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473  
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
75 80 85

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521  
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
90 95 100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569  
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
105 110 115

gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617  
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
120 125 130 135

tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat 665  
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn  
140 145 150

ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc 713  
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr  
155 160 165

tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt 761  
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser

170

175

180

aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att 809  
 Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile  
 185 190 195

gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc 857  
 Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro  
 200 205 210 215

ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt 905  
 Leu Val Ile Phe Phe Gly Leu Cys Leu Ser Leu Leu Phe Ile Gly  
 220 225 230

tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt 953  
 Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val  
 235 240 245

tgt ggg aaa tcg aca cct gaa aaa gag ggg gag ctt gaa gga act act 1001  
 Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr  
 250 255 260

act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc 1049  
 Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe  
 265 270 275

acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc 1097  
 Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser  
 280 285 290 295

agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc 1145  
 Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg  
 300 305 310

aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca 1193  
 Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr  
 315 320 325

gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac 1241  
 Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp  
 330 335 340

agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg 1289  
 Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu  
 345 350 355

tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aaggattc 1334  
 Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp  
 360 365 370

<210> 12  
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 <213> Artificial Sequence

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<223> Description of Artificial Sequence: cDNA insert of  
lambdaTNF-BP15 and pTNF-BP15 vectors

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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
35 40 45  
  
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60  
  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
65 70 75 80  
  
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95  
  
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110  
  
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125  
  
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140  
  
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160  
  
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175  
  
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190  
  
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
195 200 205  
  
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
210 215 220  
  
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
225 230 235 240  
  
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255  
  
Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270  
  
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
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Leu Arg Trp  
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<210> 13  
<211> 6414  
<212> DNA  
<213> Artificial Sequence

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<222> (344)  
<223> "n" can be a, g, c, or t

<220>  
<221> unsure  
<222> (4157)  
<223> "n" can be a, g, c, or t

<220>  
<221> unsure  
<222> (5135)  
<223> "n" can be a, g, c, or t

<220>  
<221> unsure  
<222> (6255)  
<223> "n" can be a, g, c, or t

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caacgacccc cgccccattga cgtcaataat gacgtatgtt cccatagtaa cgccaatagg 180  
gactttccat tgacgtcaat gggtgagta tttacggtaa actgcccact tggcagtaca 240



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gcggccacgc cggactggc ggggcccggc tggtgaggc ggagtctgac ctcgtggagg 2160  
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ggacagaatt aatatagttc tcagtagaga gctcaaggaa ccaccacaag gagctcattt 2880  
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agtggacatg gtttgatag ttggaggcag ttccgttac aaggaagcca tgaatcagcc 3000  
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cccagaaatt gattggaga aatataaaact tctccagag tacccagggg tccttctga 3120  
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gataagtcgt gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg 6120  
tcgggctgaa cgggggggttc gtgcacacag cccagctgg agcgaacgac ctacaccgaa 6180  
ctgagatacc tacagcgtga gcattgagaa agcgccacgc ttcccgaagg gagaaaggcg 6240  
gacaggtatc cggtnagcgg cagggtcgga acaggagagc gcacgaggga gcttccaggg 6300  
ggaaacgcct ggtatctta tagtctgtc gggttcgcc acctctgact tgagcgtcga 6360  
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<210> 14  
<211> 2173  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (245)..(1630)

<220>  
<223> Description of Artificial Sequence: raTNF-R8

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gggctcacgc tgccaaacacc cggccaccc ggtccgatcg tcttacttca ttcaccagcg 180  
ttgccaattt ctgcctgtc cccagccccca atgggggagt gagagaggcc actgccggcc 240

ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg tca ctg gtg ctc	289
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Ser Leu Val Leu	
1 5 10 15	
ctg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt	337
Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val	
20 25 30	
cct tct ctt ggt gac cgg gag aag agg gat aat ttg tgt ccc cag gga	385
Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly	
35 40 45	
aag tat gcc cat cca aag aat aat tcc atc tgc tgc acc aag tgc cac	433
Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His	
50 55 60	
aaa gga acc tac ttg gtg agt gac tgt cca agc cca ggg cag gaa aca	481
Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr	
65 70 75	
gtc tgc gag ctc tct cat aaa ggc acc ttt aca gct tcg cag aac cac	529
Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His	
80 85 90 95	
gtc aga cag tgt ctc agt tgc aag aca tgt cgg aaa gaa atg ttc cag	577
Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln	
100 105 110	
gtg gag att tct cct tgc aaa gct gac atg gac acc gtg tgt ggc tgc	625
Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys	
115 120 125	
aag aag aac caa ttc cag cgc tac ctg agt gag acg cat ttc cag tgt	673
Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys	
130 135 140	
gtg gac tgc agc ccc tgc ttc aat ggc acc gtg aca atc ccc tgt aag	721
Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys	
145 150 155	
gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc	769
Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser	
160 165 170 175	
gga aat gag tgc acc cct tgc agc cac tgc aag aaa aat cag gaa tgt	817
Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys	
180 185 190	
atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac	865
Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp	
195 200 205	
tca ggt act gcc gtg ctg ttg cct ctg gtt atc ttc cta ggt ctt tgc	913
Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys	
210 215 220	
ctt tta ttc ttt atc tgc atc agt cta ctg tgc cga tat ccc cag tgg	961

Leu	Leu	Phe	Phe	Ile	Cys	Ile	Ser	Leu	Leu	Cys	Arg	Tyr	Pro	Gln	Trp			
225								230							235			
agg	ccc	agg	gtc	tac	tcc	atc	att	tgt	agg	gat	tca	gct	cct	gtc	aaa	1009		
Arg	Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys			
240								245							250	255		
gag	gtg	gag	ggt	gaa	gga	att	gtt	act	aag	ccc	cta	act	cca	gcc	tct	1057		
Glu	Val	Glu	Gly	Glu	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser			
						260			265			270						
atc	cca	gcc	ttc	agc	ccc	aac	ccc	ggc	ttc	aac	ccc	act	ctg	ggc	ttc	1105		
Ile	Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe			
						275			280			285						
agc	acc	acc	cca	cgc	ttc	agt	cat	cct	gtc	tcc	agt	acc	ccc	atc	agc	1153		
Ser	Thr	Thr	Pro	Arg	Phe	Ser	His	Pro	Val	Ser	Ser	Thr	Pro	Ile	Ser			
						290			295			300						
ccc	gtc	ttc	ggt	cct	agt	aac	tgg	cac	aac	ttc	gtg	cca	cct	gta	aga	1201		
Pro	Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val	Pro	Pro	Val	Arg			
						305			310			315						
gag	gtg	gtc	cca	acc	cag	ggt	gct	gac	cct	ctc	ctc	tac	gga	tcc	ctc	1249		
Glu	Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu			
						320			325			330			335			
aac	cct	gtg	cca	atc	ccc	gcc	cct	gtt	cg	aaa	tgg	gaa	gac	gtc	gtc	1297		
Asn	Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val			
						340			345			350						
gcg	gcc	cag	cca	caa	cgg	ctt	gac	act	gca	gac	cct	g	atg	ctg	tat	1345		
Ala	Ala	Gln	Pro	Gln	Arg	Leu	Asp	Thr	Ala	Asp	Pro	Ala	Met	Leu	Tyr			
						355			360			365						
gct	gtg	gtg	gat	ggc	gtg	cct	ccg	aca	cgc	tgg	aag	gag	ttc	atg	cg	1393		
Ala	Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg			
						370			375			380						
ctc	ctg	ggg	ctg	agc	gag	cac	gag	atc	gag	cg	ttg	gag	ctg	cag	aac	1441		
Leu	Leu	Gly	Leu	Ser	Glu	His	Glu	Ile	Glu	Arg	Leu	Glu	Leu	Gln	Asn			
						385			390			395						
ggg	cgt	tgc	ctc	cgc	gag	gct	cat	tac	agc	atg	ctg	gaa	gcc	tgg	cg	1489		
Gly	Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg			
						400			405			410			415			
cgc	cgc	aca	ccg	cga	cac	gag	gcc	acg	ctg	gac	gta	gtg	ggc	cgc	gt	1537		
Arg	Arg	Thr	Pro	Arg	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val			
						420			425			430						
ctt	tgc	gac	atg	aac	ctg	cgt	ggc	tgc	ctg	gag	aac	atc	cgc	gag	act	1585		
Leu	Cys	Asp	Met	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr			
						435			440			445						
cta	gaa	agc	cct	gcc	cac	tcg	tcc	acg	acc	cac	ctc	ccg	cga	taa		1630		
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg					

450

455

460

ggccacacccc ccacacctcagg aacgggactc gaaggaccat cctgctagat gcccctgcttc 1690  
cctgtgaacc tcctctttgg tcctcttaggg ggcaggctcg atctggcagg ctgcgtctgg 1750  
cagccacttc cttggtgcta ccgacttgggt gtacatacgct tttcccagct gccgaggaca 1810  
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ggtgccaaaaa gccaggagag gtgattgtgg agaaaaagca caatctatct gataccact 1930  
tggatgcaa ggacccaaac aaagcttctc agggcctcct cagttgattt ctggccctt 1990  
ttcacagtag ataaaaacagt cttgttattt attatatcac actaatggat gaacggttga 2050  
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ttc 2173

<210> 15

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: raTNF-R8

<400> 15

Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu  
1 5 10 15

Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro  
20 25 30

Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys  
35 40 45

Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val  
65 70 75 80

Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val  
85 90 95

Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val  
100 105 110

Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys  
115 120 125

Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys Val

130 135 140  
Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu  
145 150 155 160  
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly  
165 170 175  
Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met  
180 185 190  
Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser  
195 200 205  
Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu  
210 215 220  
Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg  
225 230 235 240  
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu  
245 250 255  
Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile  
260 265 270  
Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu Gly Phe Ser  
275 280 285  
Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr Pro Ile Ser Pro  
290 295 300  
Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu  
305 310 315 320  
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn  
325 330 335  
Pro Val Pro Ile Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala  
340 345 350  
Ala Gln Pro Gln Arg Leu Asp Thr Ala Asp Pro Ala Met Leu Tyr Ala  
355 360 365  
Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu Phe Met Arg Leu  
370 375 380  
Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly  
385 390 395 400  
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg  
405 410 415  
Arg Thr Pro Arg His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu  
420 425 430  
Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu

435

440

445

Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg  
 450                    455                    460

<210> 16  
<211> 2141  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (213)..(1580)

<220>  
<223> Description of Artificial Sequence: human TNF-R in  
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ctggacagac cgagtcccg 180  
gagccccag cactgccgct gccacactgc cctgagccca 180  
katggggag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233  
Met Gly Leu Ser Thr Val Pro  
1                        5

gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281  
Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr  
10                      15                      20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329  
Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys  
25                      30                      35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377  
Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn  
40                      45                      50                      55

tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425  
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
60                      65                      70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473  
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
75                      80                      85

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521  
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
90                      95                      100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569  
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
105                      110                      115

gac	cgg	gac	acc	gtg	tgt	ggc	tgc	agg	aag	aac	cag	tac	cgg	cat	tat	617	
Asp		Arg		Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr
120							125					130				135	
tgg	agt	gaa	aac	ctt	ttc	cag	tgc	ttc	aat	tgc	agc	ctc	tgc	ctc	aat	665	
Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn		
							140				145				150		
ggg	acc	gtg	cac	ctc	tcc	tgc	cag	gag	aaa	cag	aac	acc	gtg	tgc	acc	713	
Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr		
							155				160				165		
tgc	cat	gca	ggt	ttc	ttt	cta	aga	gaa	aac	gag	tgt	gtc	tcc	tgt	agt	761	
Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser		
							170				175				180		
aac	tgt	aag	aaa	agc	ctg	gag	tgc	acg	aag	ttg	tgc	cta	ccc	cag	att	809	
Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile		
							185				190				195		
gag	aat	gtt	aag	ggc	act	gag	gac	tca	ggc	acc	aca	gtg	ctg	ttg	ccc	857	
Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	Gly	Thr	Thr	Val	Leu	Leu	Pro		
							200				205				215		
ctg	gtc	att	ttc	ttt	ggt	ctt	tgc	ctt	tta	tcc	ctc	ctc	ttc	att	ggt	905	
Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	Leu	Ser	Leu	Leu	Phe	Ile	Gly		
							220				225				230		
tta	atg	tat	cgc	tac	caa	cgg	tgg	aag	tcc	aag	ctc	tac	tcc	att	gtt	953	
Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	Ser	Lys	Leu	Tyr	Ser	Ile	Val		
							235				240				245		
tgt	ggg	aaa	tcg	aca	cct	gaa	aaa	gag	ggg	gag	ctt	gaa	gga	act	act	1001	
Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr		
							250				255				260		
act	aag	ccc	ctg	gcc	cca	aac	cca	agc	ttc	agt	ccc	act	cca	ggc	ttc	1049	
Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser	Phe	Ser	Pro	Thr	Pro	Gly	Phe		
							265				270				275		
acc	ccc	acc	ctg	ggc	ttc	agt	ccc	gtg	ccc	agt	tcc	acc	ttc	acc	tcc	1097	
Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val	Pro	Ser	Ser	Thr	Phe	Thr	Ser		
							280				285				290		
300																295	
agc	tcc	acc	tat	acc	ccc	ggt	gac	tgt	ccc	aac	ttt	gcg	gct	ccc	cgc	1145	
Ser	Ser	Thr	Tyr	Thr	Pro	Gly	Asp	Cys	Pro	Asn	Phe	Ala	Ala	Pro	Arg		
305																	
310																	
aga	gag	gtg	gca	cca	ccc	tat	cag	ggg	gct	gac	ccc	atc	ttt	gcg	aca	1193	
Arg	Glu	Val	Ala	Pro	Pro	Tyr	Gln	Gly	Ala	Asp	Pro	Ile	Leu	Ala	Thr		
							315				320				325		
gcc	ctc	gcc	tcc	gac	ccc	atc	ccc	aac	ccc	ctt	cag	aag	tgg	gag	gac	1241	
Ala	Leu	Ala	Ser	Asp	Pro	Ile	Pro	Asn	Pro	Leu	Gln	Lys	Trp	Glu	Asp		
							330				335				340		

agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg		1289	
Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu			
345	350	355	
tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aag gaa ttc gtg		1337	
Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val			
360	365	370	375
cgg cgc cta ggg ctg agc gac cac gag atc gat cgg ctg gag ctg cag		1385	
Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln			
380	385	390	
aac ggg cgc tgc ctg cgc gag gcg caa tac agc atg ctg gcg acc tgg		1433	
Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp			
395	400	405	
agg cgg cgc acg ccg cgg cgc gag gcc acg ctg gag ctg ctg gga cgc		1481	
Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg			
410	415	420	
gtg ctc cgc gac atg gac ctg ctg ggc tgc ctg gag gac atc gag gag		1529	
Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu			
425	430	435	
gcg ctt tgc ggc ccc gcc ccc ctc ccg ccc gcg ccc agt ctt ctc aga		1577	
Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg			
440	445	450	455
tga ggctgcgccc ctgcgggcag ctctaaggac cgtcctgcga gatgccttc		1630	
caacccccact tttttctgga aaggaggggt cctgcagggg caagcaggag ctagcagccg		1690	
cctacttggt gctaaccctt cgatgtacat agctttctc agctgcctgc gcgcgcgcga		1750	
cagtcagcgc tgtgcgcgcg gagagaggtg cggcgtggc tcaagagcct gagtggtgg		1810	
tttgcgagga tgagggacgc tatgcctcat gcccgtttt ggtgtcctca ccagcaaggc		1870	
tgctcggggg cccctggggtc gtccctgagc cttttcaca gtgcataagc agttttttt		1930	
gtttttgttt tgttttgttt tgtttttaaa tcaatcatgt tacactaata gaaaacttggc		1990	
actcctgtgc cctctgcctg gacaaggcaca tagcaagctg aactgtccta aggcaaggc		2050	
gaggcacggaa caatggggcc ttcaagctgga gctgtggact tttgtacata cactaaaatt		2110	
ctgaagttaa aaaaaaaaaaaa aaaaggaatt c		2141	

<210> 17  
<211> 455  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: human TNF-R in

## 1TNF-R2

<400> 17  
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln Asp Thr Asp  
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255

Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
420 425 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
435 440 445

Pro Ala Pro Ser Leu Leu Arg  
450 455

<210> 18  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(main sequence)

<220>  
<221> UNSURE  
<222> (4)  
<223> Identity of "Xaa" could not be determined.

<400> 18  
Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln  
1 5 10

<210> 19  
<211> 9  
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(sudsidiary sequence)

<220>

<221> UNSURE

<222> (7)

<223> Identity of "Xaa" could not be determined.

<400> 19

Leu Val Pro His Leu Gly Xaa Arg Glu  
1 5

<210> 20

<211> 151

<212> DNA

<213> Homo sapiens

<400> 20

caggggaaaa tattcacccct caaataattc gatggctgt accaagtgcc acaaaggaaa 60

ctacttgtac aatgactgtc caggcccggg gcaggatacg gactgcaggg agtgtgagag 120

cggctccttc acagcctcag aaaacaacaa g 151

<210> 21

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 21

Asp Ser Val Cys Pro Gln Gly Lys  
1 5

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>

<221> UNSURE

<222> (1)...(2)

<223> Identity of "Xaa" could not be determined.

<400> 22  
Xaa Xaa Leu Ser Cys Ser Lys  
1 5

<210> 23  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 23  
Asp Thr Val Cys Gly Cys Arg  
1 5

<210> 24  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 24  
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys  
1 5 10

<210> 25  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 25  
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys  
1 5 10

<210> 26  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<220>  
<221> UNSURE  
<222> (6)  
<223> Identity of "Xaa" could not be determined.

<220>  
<221> UNSURE  
<222> (10)..(12)  
<223> Identity of "Xaa" could not be determined.

<400> 26  
Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys  
1 5 10

<210> 27  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 27  
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
1 5 10

<210> 28  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 28  
Leu Val Pro His Leu Gly Asp Arg  
1 5

<210> 29  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 29  
Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg  
1 5 10 15

<210> 30  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 30  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
1 5 10

<210> 31  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<220>  
<221> UNSURE  
<222> (9)..(11)  
<223> Identity of "Xaa" could not be determined.

<400> 31  
Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp  
1 5 10

<210> 32  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 32  
Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp  
1 5 10 15  
  
Thr Val Cys Gly  
20

<210> 33  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic

cleavage peptide

<220>  
<221> UNSURE  
<222> (6)  
<223> Identity of "Xaa" could not be determined.

<220>  
<221> UNSURE  
<222> (18)  
<223> Identity of "Xaa" could not be determined.

<400> 33  
Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
1 5 10 15

Gly Xaa Tyr

<210> 34  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>  
<221> UNSURE  
<222> (16)..(17)  
<223> Identity of "Xaa" could not be determined.

<400> 34  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Xaa  
1 5 10 15

Xaa Arg

<210> 35  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 35  
Leu Cys Leu Pro Gln Ile Glu Asn  
1 5

<210> 36

<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<220>  
<221> UNSURE  
<222> (7)  
<223> Identity of "Xaa" could not be determined.

<400> 36  
Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg  
1 5 10

<210> 37  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 37  
Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn  
1 5 10

<210> 38  
<211> 13  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 38  
Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln  
1 5 10

<210> 39  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 39  
Gln Gly Lys Tyr Ile His Pro

<210> 40  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 40  
caaggtaaat atattcatcc 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 41  
cagggttaagt acatccatcc 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 42  
caaggtaaat atatacatcc 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 43  
caaggcaaat atattcatcc 20

<210> 44  
<211> 20

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 44  
caggcaagt acatccaccc

20

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 45  
caaggcaaat atatacatcc

20

<210> 46  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 46  
caaggaaaat atattcatcc

20

<210> 47  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 47  
cagggaaagt acatccaccc

20

<210> 48  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Hybridization

probe

<400> 48  
caaggaaaat atatacatcc 20

<210> 49  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 49  
caagggaaat atattcatcc 20

<210> 50  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 50  
caggggaagt acatccaccc 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 51  
caaggaaaat atatacatcc 20

<210> 52  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 52  
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
1 5 10

<210> 53  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 53  
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys  
1 5 10

<210> 54  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 54  
Phe Thr Ala Ser Glu Asn Asn Lys  
1 5

<210> 55  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 55  
Phe Thr Ala Ser Cys Asn Asn Lys  
1 5

<210> 56  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 56  
aaatgacgga gactcttgtt gttccttaggg 30

<210> 57  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 57  
aagtggcgta gtctttgtt gttcctaggg 30

<210> 58  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 58  
aaatgtcgg aactcttgtt gttcctaggg 30

<210> 59  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 59  
aaatgacggt cactcttgtt gttcctaggg 30

<210> 60  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 60  
aagtggcggt ctctttgtt gttcctaggg 30

<210> 61  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 61  
aaatgtcggg cactcttgtt gttccttaggg 30

<210> 62  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 62  
aaatgacgga gaacatttgtt gttccttaggg 30

<210> 63  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 63  
aagtggcgta gtacttttgtt gttccttaggg 30

<210> 64  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 64  
aaatgtcggg gaacatttgtt gttccttaggg 30

<210> 65  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization probe

<400> 65

aaatgacggt caacattgtt gttcctaggg	30
<210> 66	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Hybridization probe	
<400> 66	
aaatggcggt ctactttgtt gttcctaggg	30
<210> 67	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Hybridization probe	
<400> 67	
aaatgtcggt caacattgtt gttcctaggg	30
<210> 68	
<211> 158	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (1)...(153)	
<400> 68	
cag ggg aaa tat att cac cct caa aat aat tcg att tgc tgt acc aag	48
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys	
1                         5                         10                         15	
tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag	96
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln	
20                         25                         30	
gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa	144
Asp Thr Asp Cys Arg Glu Cys Ser Gly Ser Phe Thr Ala Ser Glu	
35                         40                         45	
aac aac aag gatcc	158
Asn Asn Lys	
50	
<210> 69	

<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 69  
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys  
1 5 10 15  
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
20 25 30  
Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu  
35 40 45  
Asn Asn Lys  
50

<210> 70  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1786

<400> 70  
ggaattcagc ctgaatggcg aatggg 26

<210> 71  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1729

<400> 71  
cctcgagcgt tgctggcggtt tttcc 25

<210> 72  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1733

<400> 72  
ggtcgacatt gattattgac tag 23

<210> 73  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1734

<400> 73  
ggaattccct aggaatacag cgg 23

<210> 74  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1751

<400> 74  
gtacttgaac tcgttcctg 19

<210> 75  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1857

<400> 75  
ggcaaggcgca gcagccgg 18

<210> 76  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1823

<400> 76  
agcttctgca ggtcgacatc gatggatcgg tacctcgagc ggccgcgaat tct 53

<210> 77  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1829

<400> 77  
ctagagaatt cgcggccgct cgaggtaccc gatccatcga tgtcgacctg caga 54

<210> 78  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1820

<400> 78  
agctctagag attcgccggcc gctcgaggta ccggatccat cgatgtcgac ctgcagaagc 60  
ttg 63

<210> 79  
<211> 64  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1821

<400> 79  
ctagcaagct tctgcaggta gacatcgatg gatccggta ctcgagcggc cgcgaattct 60  
ctag 64

<210> 80  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 80  
caggatccga gtctcaaccc tcaac 25

<210> 81  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-1929

<400> 81  
ggaaattcct tatcaattct caatctgggg taggcacaac ttc 43

<210> 82  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-2452

<400> 82  
cacagtcgac ttacatgtc ttctgacaca actgtgttca ctagcaacct caaacagaca 60  
ccatgggcct ctccaccgtg c 81

<210> 83  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1922

<400> 83  
gaggctgcaa ttgaagc 17

<210> 84  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-2316

<400> 84  
attcggtgcgg cgccctag 17

<210> 85  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-2467

<400> 85  
gtcggttagca ccaagga

17

<210> 86  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 86  
gttttcccgag tcacgac

17

<210> 87  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer EBI-2112

<400> 87  
gtccaattat gtcacaccc

18